

SEQUENCE LISTING

(1) GENERAL INFORMATION:

Sub A) (i) APPLICANT: BURKS, A. Wesley, HELM, Ricki M., COCKRELL, Gael, BANNON, Gary A., STANLEY, J. Steven, SHIN, David S., SAMPSON, Hugh, COMPADRE, Cesar M., HUANG, Shau K., MALEKI, Soheila J., KOPPER, Randall A.

(ii) TITLE OF INVENTION: TERTIARY STRUCTURE OF PEANUT ALLERGEN ARA H 1

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Head, Johnson & Kachigian

(B) STREET: 112 W. Center Street, Suite 230

(C) CITY: Fayetteville

(D) STATE: Arkansas AR

(E) COUNTRY: United States of America

(F) ZIP: 72701

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: MS-DOS 6.2

(D) SOFTWARE: Word Perfect 6.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 11 March 1999

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/077,763

(B) FILING DATE: 12 March 1998

(C) APPLICATION NUMBER:

(D) FILING DATE:

(viii) ATTORNEY/ACCT INFORMATION:

- (A) NAME: Alexander, Daniel R.
- (B) REGISTRATION NUMBER: 32,604
- (C) REFERENCE/DOCKET NUMBER: ARK00898103A

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (501) 582-9111
- (B) TELEFAX: (501) 521-4931
- (C) TELEX: Not applicable

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acid residues
- (B) TYPE: Amino acid sequence
- (C) STRANDEDNESS: Not applicable
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

- (A) DESCRIPTION: 23 N-terminal amino acid residue sequence of a 14 kD protein/allergen isolated from a crude extract of peanuts (Arachis hypogaea L.) identified as Ara h 3 (IUIS/WHO)

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: Not applicable

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arachis hypogaea L.
- (B) STRAIN: Southeastern runners
- (C) INDIVIDUAL ISOLATE: Commercial lots North Carolina State Univ.
- (D) DEVELOPMENT STAGE: Mature raw peanuts
- (E) HAPLOTYPE: Not applicable
- (F) TISSUE TYPE: Mature peanuts
- (G) CELL TYPE: Not applicable
- (H) CELL LINE: Not applicable

(I) ORGANISM: Not applicable.

(vii) IMMEDIATE SOURCE: Crude soluble whole peanut extract

(A) LIBRARY: Not applicable

(B) CLONE: Not applicable

(viii) POSITION IN GENOME: Not applicable

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION: Not registered

(C) IDENTIFICATION METHOD: Not completed

(D) OTHER INFORMATION: Ara h 3 allergen isolated from crude extract of Arachis hypogaea L with an apparent molecular wt of 14 kD that binds to IgE in human serum from patients with peanut immediate hypersensitivity

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Ile	Ser	Phe	Arg	Gln	Gln	Pro	Glu	Glu	Asn	Ala	X	Gln	Phe
1					5							10	
Arg	Leu	Asn	Ala	Gln	Arg	Pro	Asp						
					20								

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acid residues

- (B) TYPE: Amino acid sequence
- (C) STRANDEDNESS: Not applicable
- (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (A) DESCRIPTION: 15 N-terminal amino acid residue sequence of a 15 kD protein/allergen isolated from a crude extract of peanuts (*Arachis hypogaea* L.) identified as Ara h 4 (IUIS/WHO)
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: Not applicable
- (v) FRAGMENT TYPE: N-terminal fragment
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Arachis hypogaea* L.
- (B) STRAIN: Southeastern runners
- (C) INDIVIDUAL ISOLATE: Commercial lots North Carolina State Univ.
- (D) DEVELOPMENT STAGE: Mature raw peanuts
- (E) HAPLOTYPE: Not applicable
- (F) TISSUE TYPE: Mature peanuts
- (G) CELL TYPE: Not applicable
- (H) CELL LINE: Not applicable
- (I) ORGANELLE: Not applicable
- (vii) IMMEDIATE SOURCE: Crude soluble whole peanut extract
- (A) LIBRARY: Not applicable
- (B) CLONE: Not applicable
- (viii) POSITION IN GENOME: Not applicable
- (ix) FEATURE:
- (A) NAME/KEY:
- (B) LOCATION: Not registered
- (C) IDENTIFICATION METHOD: Not completed
- (D) OTHER INFORMATION: Ara h 4 allergen isolated from crude extract of *Arachis hypogaea* L with an apparent molecular wt of 15 kD that binds to IgE in human serum from patients with peanut immediate hypersensitivity

(x) PUBLICATION INFORMATION:

- (A) AUTHORS:
- (B) TITLE:
- (C) JOURNAL:
- (D) VOLUME:
- (E) ISSUE:
- (F) PAGES:
- (G) DATE:
- (H) DOCUMENT NUMBER:
- (I) FILING DATE:
- (J) PUBLICATION DATE:
- (K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Arg Glu Phe Ser X Glu Gly Glu His Gly Arg Arg Glu Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acid residues
- (B) TYPE: Amino acid sequence
- (C) STRANDEDNESS: Not applicable
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

- (A) DESCRIPTION: 20 N-terminal amino acid residue sequence of a 10 kD protein/allergen (lower band) isolated from a crud extract of peanuts (Arachis hypogaea L.) identified as Ara h 5 (IUIS/WHO)

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: Not applicable

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arachis hypogaea L.
- (B) STRAIN: Southeastern runners

(C) INDIVIDUAL ISOLATE: Commercial lots North Carolina State Univ.

(D) DEVELOPMENT STAGE: Mature raw peanuts

(E) HAPLOTYPE: Not applicable

(F) TISSUE TYPE: Mature peanuts

(G) CELL TYPE: Not applicable

(H) CELL LINE: Not applicable

(I) ORGANELLE: Not applicable

(vii) IMMEDIATE SOURCE: Crude soluble whole peanut extract

(A) LIBRARY: Not applicable

(B) CLONE: Not applicable

(viii) POSITION IN GENOME: Not applicable

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION: Not registered

(C) IDENTIFICATION METHOD: Not completed

(D) OTHER INFORMATION: Ara h 5 allergen isolated from crude extract of *Arachis hypogaea* L with an apparent molecular wt of 10 kD that binds to IgE in human serum from patients with peanut immediate hypersensitivity

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ser	Thr	Arg	Ser	Ser	Asp	Gln	Gln	Gln	Arg	X	X	Asp	Glu	Le
1					5								10	
Asn	Glu	Met	X	Asn										
					20									

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:
- (B) TYPE: Amino acid sequence
- (C) STRANDEDNESS: Not applicable
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Glycoprotein

(A) DESCRIPTION:

Ara h 3 (IUIS/WHO nomenclature)

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: Not applicable

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arachis hypogaea L.
- (B) STRAIN: Southeastern runners
- (C) INDIVIDUAL ISOLATE: Commercial lots North Carolina State Univ.
- (D) DEVELOPMENT STAGE: Mature raw peanuts
- (E) HAPLOTYPE: Not applicable
- (F) TISSUE TYPE: Mature peanuts
- (G) CELL TYPE: Not applicable
- (H) CELL LINE: Not applicable
- (I) ORGANELLE: Not applicable

(vii) IMMEDIATE SOURCE: Crude soluble whole peanut extract

(A) LIBRARY: Not applicable

(B) CLONE: Not applicable

(viii) POSITION IN GENOME: Not applicable

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION: Not registered

(C) IDENTIFICATION METHOD: Not completed

(D) OTHER INFORMATION: Ara h 3 allergen isolated from
crude extract of Arachis hypogaea L

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NUMBER:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

1 S F R Q Q P E E N A C Q F Q R L N A
CGG CAG CAA CCG GAG GAG AAC GCG TGC CAG TTC CAG CGC CTC AAT GCG C

25 R I E S E G G Y I E T W N P N N Q E F
CGC ATT GAA TCA GAG GGC GGT TAC ATT GAG ACT TGG AAC CCC AAC AAC CAG GAG TTC G

49 A L S R L V L R R N A L R R P F Y S N
GCC CTC TCT CGC TTA GTC CTC CGC CGC AAC GCC CTT CGT AGG CCT TTC TAC TCC AAT G

73 F I Q Q G R G Y F G L I F P G C P R H
TTC ATC CAG CAA GGA AGG GGA TAC TTT GGG TTG ATA TTC CCT GGT TGT CCT AGA CAC T

97 T Q G R R S Q S Q R P P R R L Q G E D
ACA CAA GGT CGT CGA TCT CAG TCC CAA AGA CCA CCA AGA CGT CTC CAA GGA GAA GAC C

121 R D S H Q K V H R F D E G D L I A V P
CGA GAT AGT CAC CAG AAG GTG CAC CGT TTC GAT GAG GGT GAT CTC ATT GCA GTT CCC

145 W L Y N D H D T D V V A V S L T D T N
TGG CTC TAC AAC GAC CAC GAC ACT GAT GTT GTT GCT GTT TCT CTT ACT GAC ACC AAC

169 L D Q F P R R F N L A G N T E Q E F L

	CTT	GAT	CAG	TTC	CC	GG	AGA	TTC	AAT	TTG	GCT	GG	AAC	ACG	GAG	CAA	GAG	TTC	TTA
193	S	R	Q	S	R	R	R	S	L	P	Y	S	P	Y	S	P	Q	S	Q
	AGC	AGA	CAA	AGC	AGA	CGA	AGA	AGC	TTA	CCA	TAT	AGC	CCA	TAC	AGC	CCG	CAA	AGT	CAG
217	R	E	F	S	P	R	G	Q	H	S	R	R	E	R	A	G	Q	E	E
	CGT	GAA	TTT	AGC	CCT	CGA	GGA	CAG	CAC	AGC	CGC	AGA	GAA	CGA	GCA	GGA	CAA	GAA	GAA
241	N	I	F	S	G	F	T	P	E	F	L	E	Q	A	F	Q	V	D	D
	AAC	ATC	TTC	AGC	GGC	TTC	ACG	CCG	GAG	TTC	CTG	GAA	CAA	GCC	TTC	CAG	GTT	GAC	GAC
265	N	L	R	G	E	T	E	S	E	E	E	G	A	I	V	T	V	R	G
	AAC	CTA	AGA	GGC	GAG	ACC	GAG	AGT	GAA	GAA	GAG	GGA	GCC	ATT	GTG	ACA	GTG	AGG	GGA
289	S	P	D	R	K	R	R	A	D	E	E	E	E	Y	D	E	D	E	Y
	AGC	CCA	GAT	AGA	AAG	AGA	CGT	GCC	GAC	GAA	GAA	GAG	GAA	TAC	GAT	GAA	GAT	GAA	TAT
313	D	R	R	R	G	R	G	S	R	G	R	G	N	G	I	E	E	T	I
	GAT	AGA	AGG	CGT	GGC	AGG	GGA	AGC	AGA	GGC	AGG	GGG	AAT	GGT	ATT	GAA	GAG	ACG	ATC
337	K	K	N	I	G	R	N	R	S	P	D	I	Y	N	P	Q	A	G	S
	AAA	AAG	AAC	ATT	GGT	AGA	AAC	AGA	TCC	CCT	GAC	ATC	TAC	AAC	CCT	CAA	GCT	GGT	TCA
361	D	L	N	L	L	I	L	R	W	L	G	P	S	A	E	Y	G	N	L
	GAT	CTC	AAC	CTT	CTA	ATA	CTT	AGG	TGG	CTT	GGA	CCT	AGT	GCT	GAA	TAT	GGA	AAT	CTC
385	F	V	A	H	Y	N	T	N	A	H	S	I	I	Y	R	L	R	G	R
	TTT	GTC	GCT	CAC	TAC	AAC	ACC	AAC	GCA	CAC	AGC	ATC	ATA	TAT	CGA	TTG	AGG	GGA	CGG
409	V	D	S	N	G	N	R	V	Y	D	E	E	L	Q	E	G	H	V	L
	GTG	GAC	AGC	AAC	GGC	AAC	AGA	GTG	TAC	GAC	GAG	GAG	CTT	CAA	GAG	GGT	CAC	GTG	CTT
433	F	A	V	A	G	K	S	Q	S	E	N	F	E	Y	V	A	F	K	T
	TTC	GCC	GTC	GCT	GGA	AAG	TCC	CAG	AGC	GAG	AAC	TTC	GAA	TAC	GTG	GCA	TTC	AAG	ACA
457	I	A	N	L	A	G	E	N	S	V	I	D	N	L	P	E	E	V	V
	ATA	GCC	AAC	CTC	GCC	GGT	GAA	AAC	TCC	GTC	ATA	GAT	AAC	CTG	CCG	GAG	GAG	GTG	GTT
481	L	Q	R	E	Q	A	R	Q	L	K	N	N	N	P	F	K	F	F	V
	CTC	CAA	AGG	GAG	CAG	GCA	AGC	CAG	CTT	AAG	AAC	AAC	AAC	CCC	TTC	AAG	TTC	TTC	GTT
505	S	P	R	A	V	A	*												
	TCT	CCG	AGG	GCT	GTG	GCT	TAA												

CGC	ATT	GAA	TCA	GAG	GGC	GGT	TAC	ATT	GAG	ACT	TGG	AAC	CCC	AAC	AAC	CAG	GAG	TTC	GAA
GCC	CTC	TCT	CGC	TTA	GTC	CTC	CGC	CGC	AAC	GCC	CTT	CGT	AGG	CCT	TTC	TAC	TCC	AAT	GCT
TTC	ATC	CAG	CAA	GGA	AGG	GGA	TAC	TTT	GGG	TTG	ATA	TTC	CCT	GGT	TGT	CCT	AGA	CAC	TAT
ACA	CAA	GGT	CGT	CGA	TCT	CAG	TCC	CAA	AGA	CCA	CCA	AGA	CGT	CTC	CAA	GGA	GAA	GAC	CAA
CGA	GAT	AGT	CAC	CAG	AAG	GTG	CAC	CGT	TTC	GAT	GAG	GGT	GAT	CTC	ATT	GCA	GTT	CCC	ACC
TGG	CTC	TAC	AAC	GAC	CAC	GAC	ACT	GAT	GTT	GTT	GCT	GTT	TCT	CTT	ACT	GAC	ACC	AAC	AAC
CTT	GAT	CAG	TTC	CCC	AGG	AGA	TTC	AAT	TTG	GCT	GGG	AAC	ACG	GAG	CAA	GAG	TTC	TTA	AGG
AGC	AGA	CAA	AGC	AGA	CGA	AGA	AGC	TTA	CCA	TAT	AGC	CCA	TAC	AGC	CCG	CAA	AGT	CAG	CCT
CGT	GAA	TTT	AGC	CCT	CGA	GGA	CAG	CAC	AGC	CGC	AGA	GAA	CGA	GCA	GGA	CAA	GAA	GAA	GAA
AAC	ATC	TTC	AGC	GGC	TTC	ACG	CCG	GAG	TTC	CTG	GAA	CAA	GCC	TTC	CAG	GTT	GAC	GAC	AGA
AAC	CTA	AGA	GGC	GAG	ACC	GAG	AGT	GAA	GAA	GAG	GGA	GCC	ATT	GTG	ACA	GTG	AGG	GGA	GGC
AGC	CCA	GAT	AGA	AAG	AGA	CGT	GCC	GAC	GAA	GAA	GAG	GAA	TAC	GAT	GAA	GAT	GAA	TAT	GAA
GAT	AGA	AGG	CGT	GGC	AGG	GGA	AGC	AGA	GGC	AGG	GGG	AAT	GGT	ATT	GAA	GAG	ACG	ATC	TGC
AAA	AAG	AAC	ATT	GGT	AGA	AAC	AGA	TCC	CCT	GAC	ATC	TAC	AAC	CCT	CAA	GCT	GGT	TCA	CTC
GAT	CTC	AAC	CTT	CTA	ATA	CTT	AGG	TGG	CTT	GGA	CCT	AGT	GCT	GAA	TAT	GGA	AAT	CTC	TAC
TTT	GTC	GCT	CAC	TAC	AAC	ACC	AAC	GCA	CAC	AGC	ATC	ATA	TAT	CGA	TTG	AGG	GGA	CGG	GCT
GTG	GAC	AGC	AAC	GGC	AAC	AGA	GTG	TAC	GAC	GAG	GAG	CTT	CAA	GAG	GGT	CAC	GTG	CTT	GTG
TTC	GCC	GTC	GCT	GGA	AAG	TCC	CAG	AGC	GAG	AAC	TTC	GAA	TAC	GTG	GCA	TTC	AAG	ACA	GAC
ATA	GCC	AAC	CTC	GCC	GGT	GAA	AAC	TCC	GTC	ATA	GAT	AAC	CTG	CCG	GAG	GAG	GTG	GTT	GCA
CTC	CAA	AGG	GAG	CAG	GCA	AGG	CAG	CTT	AAG	AAC	AAC	AAC	CCC	TTC	AAG	TTC	TTC	GTT	CCA
TCT	CCG	AGG	GCT	GTG	GCT	TAA													

<210> 5
 <211> 1524
 <212> DNA
 <213> Peanut

<400> 5

cggcagcaac cggaggagaa cgcgtgccag ttccagcgcc tcaatgcgca gagacctgac 60
aatcgcattg aatcagaggg cggttacatt gagacttgga accccaacaa ccaggagttc 120
gaatgcgccg gcgtcgccct ctctcgctta gtctccgcc gcaacgcctt tcgtaggcct 180
ttctactcca atgctcccca ggagatcttc atccagcaag gaaggggata ctttgggttg 240
atattccctg gttgtcctag acactatgaa gagcttcaca cacaaggctg tcgatctcag 300
tcccaaagac caccaagacg tctccaagga gaagacaaa gccaacagca acgagatagt 360
caccagaagg tgcaccgttt cgatgagggg gatctcattg cagttccac cggtgttgct 420
ttctggctct acaacgacca cgactgat gttgttgctg tttctcttac tgacaccaac 480
aacaacgaca accagcttga tcagttcccc aggagattca atttggttg gaacacggag 540
caagagttct taaggtagca gcaacaaagc agacaaagca gacgaagaag cttaccatat 600
agcccatata gcccgcaaag tcagcctaga caagaagagc gtgaatttag ccctcgagga 660
cagcacagcc gcagagaacg agcaggacaa gaagaagaaa acgaagggtg aaacatcttc 720
agcggcttca cgcgcgagtt cctggaacaa gccttcagg ttgacgacag acagatagtg 780
caaaacctaa gaggcgagac cgagagtga gaagaggag ccattgtgac agtgagggga 840
ggcctcagaa tcttgagccc agatagaaa agacgtgccg acgaagaaga ggaatacgat 900
gaagatgaat atgaatacga tgaagaggat agaaggcgtg gcaggggaag cagaggcagg 960
gggaatggta ttgaagagac gatctgcacc gcaagtgcta aaaagaacat tcgtagaaac 1020
agatccctg acatctacaa ccctcaagct ggttcactca aaactgccaa cgatctcaac 1080
cttctaatac ttaggtggct tggacctagt gctgaatatg gaaatctcta caggaatgca 1140
ttgtttgtcg ctactacaa caccaacgca cacagcatca tatatcgatt gaggggacgg 1200
gctcacgtgc aagtcgtgga cagcaacgac aacagagtgt acgacgagga gcttcaagag 1260
ggtcacgtgc ttgtggtgcc acagaacttc gccgtcgctg gaaagtcca gagcgagaac 1320
ttcgaatacg tggcattcaa gacagactca aggccagca tagccaacct cgccggtgaa 1380
aactccgtca tagataacct gccggaggag gtggttgcaa attcatatgg cctccaaagg 1440
gagcaggcaa ggcagcttaa gaacaacaac cccttcaagt tcttcgttcc accgtctcag 1500
cagtctccga gggctgtggc ttaa 1524

<210> 6

<211> 510

<212> PRT

<213> Peanut

<220>

<221> PEPTIDE

<222> (33)..(47)

<223> peptide 1

<220>

<221> PEPTIDE

<222> (240)..(254)

<223> peptide 2

<220>

<221> PEPTIDE

<222> (279)..(293)

<223> peptide 3

<220>

<221> PEPTIDE

<222> (303)..(317)

<223> peptide 4

<400> 6

Ile Ser Phe Arg Gln Gln Pro Glu Glu Asn Ala Cys Gln Phe Gln Arg

1

5

10

15

Leu Asn Ala Gln Arg Pro Asp Asn Arg Ile Glu Ser Glu Gly Gly Tyr

20

25

30

Ile Glu Thr Trp Asn Pro Asn Asn Gln Glu Phe Glu Cys Ala Gly Val
35 40 45

Ala Leu Ser Arg Leu Val Leu Arg Arg Asn Ala Leu Arg Arg Pro Phe
50 55 60

Tyr Ser Asn Ala Pro Gln Glu Ile Phe Ile Gln Gln Gly Arg Gly Tyr
65 70 75 80

Phe Gly Leu Ile Phe Pro Gly Cys Pro Arg His Tyr Glu Glu Pro His
85 90 95

Thr Gln Gly Arg Arg Ser Gln Ser Gln Arg Pro Pro Arg Arg Leu Gln
100 105 110

Gly Glu Asp Gln Ser Gln Gln Gln Arg Asp Ser His Gln Lys Val His
115 120 125

Arg Phe Asp Glu Gly Asp Leu Ile Ala Val Pro Thr Gly Val Ala Phe
130 135 140

Trp Leu Tyr Asn Asp His Asp Thr Asp Val Val Ala Val Ser Leu Thr
145 150 155 160

Asp Thr Asn Asn Asn Asp Asn Gln Leu Asp Gln Phe Pro Arg Arg Phe
165 170 175

Asn Leu Ala Gly Asn Thr Glu Gln Glu Phe Leu Arg Tyr Gln Gln Gln
180 185 190

Ser Arg Gln Ser Arg Arg Arg Ser Leu Pro Tyr Ser Pro Tyr Ser Pro
 195 200 205

Gln Ser Gln Pro Arg Gln Glu Glu Arg Glu Phe Ser Pro Arg Gly Gln
 210 215 220

His Ser Arg Arg Glu Arg Ala Gly Gln Glu Glu Glu Asn Glu Gly Gly
 225 230 235 240

Asn Ile Phe Ser Gly Phe Thr Pro Glu Phe Leu Glu Gln Ala Phe Gln
 245 250 255

Val Asp Asp Arg Gln Ile Val Gln Asn Leu Arg Gly Glu Thr Glu Ser
 260 265 270

Glu Glu Glu Gly Ala Ile Val Thr Val Arg Gly Gly Leu Arg Ile Leu
 275 280 285

Ser Pro Asp Arg Lys Arg Arg Ala Asp Glu Glu Glu Glu Tyr Asp Glu
 290 295 300

Asp Glu Tyr Glu Tyr Asp Glu Glu Asp Arg Arg Arg Gly Arg Gly Ser
 305 310 315 320

Arg Gly Arg Gly Asn Gly Ile Glu Glu Thr Ile Cys Thr Ala Ser Ala
 325 330 335

Lys Lys Asn Ile Gly Arg Asn Arg Ser Pro Asp Ile Tyr Asn Pro Gln
 340 345 350

Ala Gly Ser Leu Lys Thr	Ala Asn Asp Leu Asn Leu Leu Ile Leu Arg
355	360 365
Trp Leu Gly Leu Ser Ala Glu Tyr Gly Asn Leu Tyr Arg Asn Ala Leu	
370	375 380
Phe Val Ala His Tyr Asn Thr Asn Ala His Ser Ile Ile Tyr Arg Leu	
385	390 395 400
Arg Gly Arg Ala His Val Gln Val Val Asp Ser Asn Gly Asn Arg Val	
405	410 415
Tyr Asp Glu Glu Leu Gln Glu Gly His Val Leu Val Val Pro Gln Asn	
420	425 430
Phe Ala Val Ala Gly Lys Ser Gln Ser Glu Asn Phe Glu Tyr Val Ala	
435	440 445
Phe Lys Thr Asp Ser Arg Pro Ser Ile Ala Asn Leu Ala Gly Glu Asn	
450	455 460
Ser Val Ile Asp Asn Leu Pro Glu Glu Val Val Ala Asn Ser Tyr Gly	
465	470 475 480
Leu Gln Arg Glu Gln Ala Arg Gln Leu Lys Asn Asn Asn Pro Phe Lys	
485	490 495
Phe Phe Val Pro Pro Ser Gln Gln Ser Pro Arg Ala Val Ala	
500	505 510

<210> 7
<211>
<212> DNA
<213> Peanut

Alignment Of The Primary Amino Acid Sequences Of Ara h 1
And Phaseolin A Chain

NNPFYFPSRR FSTRYGNQNGRIRVLQRFQDQSRQFQNLQNHRIVQIEAKPNTLVLP 227
DNPFFYNSDNSWNTLFKNQYGHIRVLQRFQDQSKRLQNLEDYRLVEFRSKPETLLP

KHADADNILVIQQGQATVTVANGN NRKSFNLDEGH ALRIPSGFISYILNRH 278
QQADAELLVVRSGSAILVLVKPDDRREYFFLTSDNPIFSDHQKIPAGTIFYLVNPD

DNQNLRVAKISMPVNTPGQFEDFFPASSRDQSSYLQGFSTRNTLEAAFNAEFNEIRRV 335
PKEDLRHQLAMPVNNPQH EFFLSSTEAQQSYLQEFKSKHILEASFNSKFEEINRV

LLEENAGGEQEERGQRRWSTRSSENEGVIKVSKEHVEELTKHAKSVSKKGSEEE 391
LFEEEGQQEGV IVNIDSEIKELSKHAKSSSRKSLSKQD

GDITNPINLREGEPDLSNNFGKLFVVKPDKKNPQLQDLDMMLTCVEIKEGALMLPHF 448
NTIGNEF GNLTERTDNSLN VLISSIEMEEGALFVPHY

NSKAMVIVVVNKGTGNLELVAVRKEQQQRGRREEEEDDEDEEEEGSNREVRRYTARLK 505
YSKAIVILVVNEGEAHVELVGPKGNKETLEYE SYRAELS

EGDVFIMPAAHPVAINASSELHLLGFGINAENNHRIFLAGDKDNVIDQIE KQ 557
KDDVVFIPAAYPVAIKATSNVNFITGFGINANNNNRNLLAGKTDNVISSIGRALDGKD

AKDLAFPGSGEQVEKLIKNOKESHFVSAR 586
VLGLTFSGSGDEVMLINKQSGSYFVDAH